Figure 1: Nucleotide (SEQ ID NO: 1) and deduced amino acid sequence of human ChemR23 (AC075748)

```
  1  M   E   D   E   D   Y   N   T   S   I   S   Y   G   D   E      15
175 ATG GAG GAT GAA GAT TAC AAC ACT TCC ATC AGT TAC GGT GAT GAA     219

 16  Y   P   D   Y   L   D   S   I   V   V   L   E   D   L   S      30
220 TAC CCT GAT TAT TTA GAC TCC ATT GTG GTT TTG GAG GAC TTA TCC     264

 31  P   L   E   A   R   V   T   R   I   F   L   V   V   V   Y      45
265 CCC TTG GAA GCC AGG GTG ACC AGG ATC TTC CTG GTG GTG GTC TAC     309

 46  S   I   V   C   F   L   G   I   L   G   N   G   L   V   I      60
310 AGC ATC GTC TGC TTC CTC GGG ATT CTG GGC AAT GGT CTG GTG ATC     354

 61  I   I   A   T   F   K   M   K   K   T   V   N   M   V   W      75
355 ATC ATT GCC ACC TTC AAG ATG AAG AAG ACA GTG AAC ATG GTC TGG     399

 76  F   L   N   L   A   V   A   D   F   L   F   N   V   F   L      90
400 TTC CTC AAC CTG GCA GTG GCA GAT TTC CTG TTC AAC GTC TTC CTC     444

 91  P   I   H   I   T   Y   A   A   M   D   Y   H   W   V   F     105
445 CCA ATC CAT ATC ACC TAT GCC GCC ATG GAC TAC CAC TGG GTT TTC     489

106  G   T   A   M   C   K   I   S   N   F   L   L   I   H   N     120
490 GGG ACA GCC ATG TGC AAG ATC AGC AAC TTC CTT CTC ATC CAC AAC     534

121  M   F   T   S   V   F   L   L   T   I   I   S   S   D   R     135
535 ATG TTC ACC AGC GTC TTC CTG CTG ACC ATC ATC AGC TCT GAC CGC     579

136  C   I   S   V   L   L   P   V   W   S   Q   N   H   R   S     150
580 TGC ATC TCT GTG CTC CTC CCT GTC TGG TCC CAG AAC CAC CGC AGC     624

151  V   R   L   A   Y   M   A   C   M   V   I   W   V   L   A     165
625 GTT CGC CTG GCT TAC ATG GCC TGC ATG GTC ATC TGG GTC CTG GCT     669

166  F   F   L   S   S   P   S   L   V   F   R   D   T   A   N     180
670 TTC TTC TTG AGT TCC CCA TCT CTC GTC TTC CGG GAC ACA GCC AAC     714

181  L   H   G   K   I   S   C   F   N   N   F   S   L   S   T     195
715 CTG CAT GGG AAA ATA TCC TGC TTC AAC AAC TTC AGC CTG TCC ACA     759

196  P   G   S   S   S   W   P   T   H   S   Q   M   D   P   V     210
760 CCT GGG TCT TCC TCG TGG CCC ACT CAC TCC CAA ATG GAC CCT GTG     804

211  G   Y   S   R   H   M   V   V   T   V   T   R   F   L   C     225
805 GGG TAT AGC CGG CAC ATG GTG GTG ACT GTC ACC CGC TTC CTC TGT     849

226  G   F   L   V   P   V   L   I   I   T   A   C   Y   L   T     240
850 GGC TTC CTG GTC CCA GTC CTC ATC ATC ACA GCT TGC TAC CTC ACC     894

241  I   V   C   K   L   Q   R   N   R   L   A   K   T   K   K     255
895 ATC GTC TGC AAA CTG CAG CGC AAC CGC CTG GCC AAG ACC AAG AAG     939

256  P   F   K   I   I   V   T   I   I   I   T   F   F   L   C     270
940 CCC TTC AAG ATT ATT GTG ACC ATC ATC ATT ACC TTC TTC CTC TGC     984
```

271 W C P Y H T L N L L E L H H T 285
985 TGG TGC CCC TAC CAC ACA CTC AAC CTC CTA GAG CTC CAC CAC ACT 1029

286 A M P G S V F S L G L P L A T 300
1030 GCC ATG CCT GGC TCT GTC TTC AGC CTG GGT TTG CCC CTG GCC ACT 1074

301 A L A I A N S C M N P I L Y V 315
1075 GCC CTT GCC ATT GCC AAC AGC TGC ATG AAC CCC ATT CTG TAT GTT 1119

316 F M G Q D F K K F K V A L F S 330
1120 TTC ATG GGT CAG GAC TTC AAG AAG TTC AAG GTG GCC CTC TTC TCT 1164

331 R L V N A L S E D T G H S S Y 345
1165 CGC CTG GTC AAT GCT CTA AGT GAA GAT ACA GGC CAC TCT TCC TAC 1209

346 P S H R S F T K M S S M N E R 360
1210 CCC AGC CAT AGA AGC TTT ACC AAG ATG TCA TCA ATG AAT GAG AGG 1254

361 T S M N E R E T G M L * 372
1255 ACT TCT ATG AAT GAG AGG GAG ACC GGC ATG CTT TGA 1290

Figure 2: Amino acid sequence of human ChemR23 (371 amino acids) (SEQ ID NO 2). The seven predicted transmembrane domaines are underlined. The consensus sequence for *N*-linked glycosylation (N-X-S/T) in the N terminus is bold and the potential site of phosphorylation by PKC (S/T-X-R/K) in the C terminus is in italic.

MEDEDY**NTS**ISYGDEYPDYLDSIVVLEDLSPLEARVTRIFLVVVYSIVCFLGILGNGLVIIIAT
FKMKKTVNMVWFLNLAVADFLFNVFLPIHITYAAMDYHWVFGTAMCKISNFLLIHNMFTSVFLL
TIISSDRCISVLLPVWSQNHRSVRLAYMACMVIWVLAFFLSSPSLVFRDTANLHGKISCFNNFS
LSTPGSSSWPTHSQMDPVGYSRHMVVTVTRFLCGFLVPVLIITACYLTIVCKLQRNRLAKTKKP
FKIIVTIIITFFLCWCPYHTLNLLELHHTAMPGSVFSLGLPLATALAIANSCMNPILYVFMGQD
FKKFKVALFSRLVNALSEDTGHSSYP*SHR*SFTKMSSMNERTSMNERETGML

Figure 3: Nucleotide and deduced amino acid sequence of mouse dez (AC u79525 – SEQ ID NOs:3 and 4, respectively)

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  1 M  E  Y  D  A  Y  N  D  S  G  I  Y  D  D  E      15
265 ATG GAG TAC GAC GCT TAC AAC GAC TCC GGC ATC TAT GAT GAT GAG    309

 16 Y  S  D  G  F  G  Y  F  V  D  L  E  E  A  S      30
310 TAC TCT GAT GGC TTT GGC TAC TTT GTG GAC TTG GAG GAG GCG AGT    354

 31 P  W  E  A  K  V  A  P  V  F  L  V  V  I  Y      45
355 CCG TGG GAG GCC AAG GTG GCC CCG GTC TTC CTG GTG GTG ATC TAC    399

 46 S  L  V  C  F  L  G  L  L  G  N  G  L  V  I      60
400 AGC TTG GTG TGC TTC CTC GGT CTC CTA GGC AAC GGC CTG GTG ATT    444

 61 V  I  A  T  F  K  M  K  K  T  V  N  T  V  W      75
445 GTC ATC GCC ACC TTC AAG ATG AAG AAG ACC GTG AAC ACT GTG TGG    489

 76 F  V  N  L  A  V  A  D  F  L  F  N  I  F  L      90
490 TTT GTC AAC CTG GCT GTG GCC GAC TTC CTG TTC AAC ATC TTT TTG    534

 91 P  M  H  I  T  Y  A  A  M  D  Y  H  W  V  F     105
535 CCG ATG CAC ATC ACC TAC GCG GCC ATG GAC TAC CAC TGG GTG TTC    579

106 G  K  A  M  C  K  I  S  N  F  L  L  S  H  N     120
580 GGG AAG GCC ATG TGC AAG ATC AGC AAC TTC TTG CTC AGC CAC AAC    624

121 M  Y  T  S  V  F  L  L  T  V  I  S  F  D  R     135
625 ATG TAC ACC AGC GTC TTC CTG CTG ACT GTC ATC AGC TTT GAC CGC    669

136 C  I  S  V  L  L  P  V  W  S  Q  N  H  R  S     150
670 TGC ATC TCC GTG CTG CTC CCC GTC TGG TCC CAG AAC CAC CGC AGC    714

151 I  R  L  A  Y  M  T  C  S  A  V  W  V  L  A     165
715 ATC CGC CTG GCC TAC ATG ACC TGC TCG GCC GTC TGG GTC CTG GCT    759

166 F  F  L  S  S  P  S  L  V  F  R  D  T  A  N     180
760 TTC TTC TTG AGC TCC CCG TCC CTT GTC TTC CGG GAC ACC GCC AAC    804

181 I  H  G  K  I  T  C  F  N  N  F  S  L  A  A     195
805 ATT CAT GGG AAG ATA ACC TGC TTC AAC AAC TTC AGC TTG GCC GCG    849

196 P  E  S  S  P  H  P  A  H  S  Q  V  V  S  T     210
850 CCT GAG TCC TCC CCA CAT CCC GCC CAC TCG CAA GTA GTT TCC ACA    894

211 G  Y  S  R  H  V  A  V  T  V  T  R  F  L  C     225
895 GGG TAC AGC AGA CAC GTG GCG GTC ACT GTC ACC CGC TTC CTT TGC    939

226 G  F  L  I  P  V  F  I  I  T  A  C  Y  L  T     240
940 GGC TTC CTG ATC CCC GTC TTC ATC ATC ACG GCC TGC TAC CTT ACC    984

241 I  V  F  K  L  Q  R  N  R  L  A  K  N  K  K     255
985 ATC GTC TTC AAG CTG CAG CGC AAC CGC CTG GCC AAG AAC AAG AAG   1029

256 P  F  K  I  I  I  T  I  I  I  T  F  F  L  C     270
1030 CCC TTC AAG ATC ATC ATC ACC ATC ATC ATC ACC TTC TTC CTC TGC  1074

271 W  C  P  Y  H  T  L  Y  L  L  E  L  H  H  T     285
1075 TGG TGC CCC TAC CAC ACC CTC TAC CTG CTG GAG CTC CAC CAC ACA  1119

286 A  V  P  S  S  V  F  S  L  G  L  P  L  A  T     300
1120 GCT GTG CCA AGC TCT GTC TTC AGC CTG GGG CTA CCC CTG GCC ACG  1164
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 301 A   V   A   I   A   N   S   C   M   N   P   I   L   Y   V      315
1165 GCC GTC GCC ATC GCC AAC AGC TGC ATG AAC CCC ATT CTG TAC GTC    1209

 316 F   M   G   H   D   F   R   K   F   K   V   A   L   F   S      330
1210 TTC ATG GGC CAC GAC TTC AGA AAA TTC AAG GTG GCC CTC TTC TCC    1254

 331 R   L   A   N   A   L   S   E   D   T   G   P   S   S   Y      345
1255 CGC CTG GCC AAC GCC CTG AGT GAG GAC ACA GGC CCC TCC TCC TAC    1299

 346 P   S   H   R   S   F   T   K   M   S   S   L   N   E   K      360
1300 CCC AGT CAC AGG AGC TTC ACC AAG ATG TCG TCT TTG AAT GAG AAG    1344

 361 A   S   V   N   E   K   E   T   S   T   L   *                  372
1345 GCT TCG GTG AAT GAG AAG GAG ACC AGT ACC CTC TGA                1380
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Figure 4: Nucleotide and deduced amino acid sequence of rat G-protein coupled chemoattractant-1 (AC NM_022218 - SEQ ID Nos: 5 and 6, respectively).

```
  1  M   E   Y   E   G   Y   N   D   S   S   I   Y   G   E   E      15
  1 ATG GAG TAC GAG GGT TAC AAC GAC TCC AGC ATC TAC GGT GAG GAG      45

 16  Y   S   D   G   S   D   Y   I   V   D   L   E   E   A   G      30
 46 TAT TCT GAC GGC TCG GAC TAC ATC GTG GAC TTG GAG GAG GCG GGT      90

 31  P   L   E   A   K   V   A   E   V   F   L   V   V   I   Y      45
 91 CCA CTG GAG GCC AAG GTG GCC GAG GTC TTC CTG GTG GTA ATC TAC     135

 46  S   L   V   C   F   L   G   I   L   G   N   G   L   V   I      60
136 AGC TTG GTG TGC TTC CTC GGG ATC CTA GGC AAT GGC CTG GTG ATT     180

 61  V   I   A   T   F   K   M   K   K   T   V   N   T   V   W      75
181 GTC ATC GCC ACC TTC AAG ATG AAG AAG ACG GTG AAC ACC GTG TGG     225

 76  F   V   N   L   A   V   A   D   F   L   F   N   I   F   L      90
226 TTT GTC AAC CTG GCC GTG GCT GAC TTC CTG TTC AAC ATC TTC TTG     270

 91  P   I   H   I   T   Y   A   A   M   D   Y   H   W   V   F     105
271 CCC ATC CAC ATC ACC TAT GCC GCT ATG GAC TAC CAC TGG GTG TTC     315

106  G   K   A   M   C   K   I   S   S   F   L   L   S   H   N     120
316 GGG AAA GCC ATG TGC AAG ATT AGT AGC TTT CTG CTA AGC CAC AAC     360

121  M   Y   T   S   V   F   L   L   T   V   I   S   F   D   R     135
361 ATG TAC ACC AGC GTC TTC CTG CTC ACT GTC ATC AGC TTC GAC CGC     405

136  C   I   S   V   L   L   P   V   W   S   Q   N   H   R   S     150
406 TGC ATC TCC GTG CTC CTC CCC GTC TGG TCC CAG AAC CAC CGC AGC     450

151  V   R   L   A   Y   M   T   C   V   V   V   W   V   W   L     165
451 GTG CGT CTG GCC TAC ATG ACC TGC GTG GTT GTC TGG GTC TGG CTT     495

166  S   S   E   S   P   P   S   L   V   F   G   H   V   S   T     180
496 TCT TCT GAG TCT CCC CCG TCC CTC GTC TTC GGA CAC GTC AGC ACC     540

181  S   H   G   K   I   T   C   F   N   N   F   S   L   A   A     195
541 AGC CAC GGG AAG ATA ACC TGC TTC AAC AAC TTC AGC CTG GCG GCG     585

196  P   E   P   F   S   H   S   T   H   P   R   T   D   P   V     210
586 CCC GAG CCT TTC TCT CAT TCC ACC CAC CCG CGA ACA GAC CCG GTA     630

211  G   Y   S   R   H   V   A   V   T   V   T   R   F   L   C     225
631 GGG TAC AGC AGA CAT GTG GCG GTC ACC GTC ACC CGC TTC CTC TGT     675

226  G   F   L   I   P   V   F   I   I   T   A   C   Y   L   T     240
676 GGC TTC CTG ATC CCC GTC TTC ATC ATC ACG GCC TGT TAC CTC ACC     720

241  I   V   F   K   L   Q   R   N   R   Q   A   K   T   K   K     255
721 ATC GTC TTC AAG TTG CAG CGC AAC CGC CAG GCC AAG ACC AAG AAG     765

256  P   F   K   I   I   I   T   I   I   I   T   F   F   L   C     270
766 CCC TTC AAG ATC ATC ATC ACC ATC ATC ATC ACC TTC TTC CTC TGC     810

271  W   C   P   Y   H   T   L   Y   L   L   E   L   H   H   T     285
811 TGG TGC CCC TAC CAC ACA CTC TAC CTG CTG GAG CTC CAC CAC ACG     855

286  A   V   P   A   S   V   F   S   L   G   L   P   L   A   T     300
```

```
 856 GCT GTG CCA GCC TCT GTC TTC AGC CTG GGA CTG CCC CTG GCC ACA     900

 301  A   V   A   I   A   N   S   C   M   N   P   I   L   Y   V      315
 901 GCC GTC GCC ATC GCC AAC AGC TGT ATG AAC CCC ATC CTG TAC GTC     945

 316  F   M   G   H   D   F   K   K   F   K   V   A   L   F   S      330
 946 TTC ATG GGC CAC GAC TTC AAA AAA TTC AAG GTG GCC CTT TTC TCC     990

 331  R   L   V   N   A   L   S   E   D   T   G   P   S   S   Y      345
 991 CGC CTG GTG AAT GCC CTG AGC GAG GAC ACA GGA CCC TCC TCC TAC    1035

 346  P   S   H   R   S   F   T   K   M   S   S   L   I   E   K      360
1036 CCC AGT CAC AGG AGC TTC ACC AAG ATG TCC TCA TTG ATT GAG AAG    1080

 361  A   S   V   N   E   K   E   T   S   T   L   *                  372
1081 GCT TCA GTG AAT GAG AAA GAG ACC AGC ACC CTC TGA                1116
```

Figure 5: Alignment of ChemR23

Alignment of the amino acid sequence of ChemR23 with AT2 receptors, C3a, C5a and fMLP receptor and other chemoattractants related sequences were performed using ClustalX algorithm. Then, the dendrogram was constucted using TreeView algorithm.

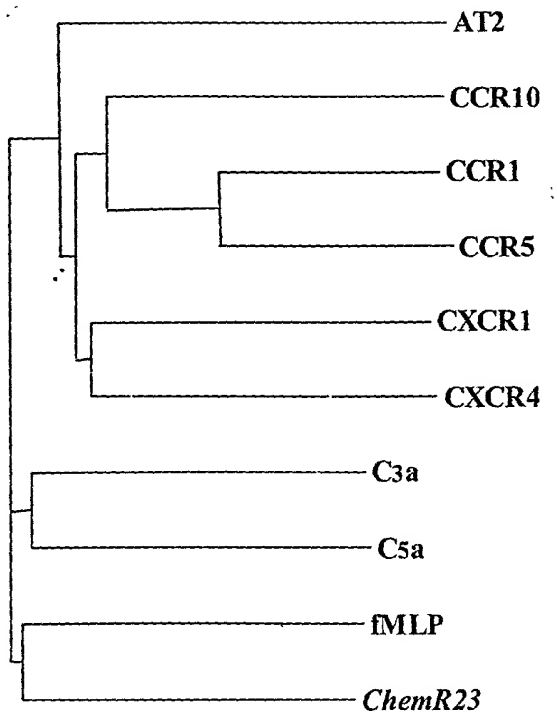

Figure 6: Nucleotide and deduced amino acid sequence of human Tig2 (AC Q99969 - SEQ ID Nos: 7 and 8, respectively)

```
  1  M   R   R   L   L   I   P   L   A   L   W   L   G   A   V     15
 97 ATG CGA CGG CTG CTG ATC CCT CTG GCC CTG TGG CTG GGT GCG GTG    141

 16  G   V   G   V   A   E   L   T   E   A   Q   R   R   G   L     30
142 GGC GTG GGC GTC GCC GAG CTC ACG GAA GCC CAG CGC CGG GGC CTG    186

 31  Q   V   A   L   E   E   F   H   K   H   P   P   V   Q   W     45
187 CAG GTG GCC CTG GAG GAA TTT CAC AAG CAC CCG CCC GTG CAG TGG    231

 46  A   F   Q   E   T   S   V   E   S   A   V   D   T   P   F     60
232 GCC TTC CAG GAG ACC AGT GTG GAG AGC GCC GTG GAC ACG CCC TTC    276

 61  P   A   G   I   F   V   R   L   E   F   K   L   Q   Q   T     75
277 CCA GCT GGA ATA TTT GTG AGG CTG GAA TTT AAG CTG CAG CAG ACA    321

 76  S   C   R   K   R   D   W   K   K   P   E   C   K   V   R     90
322 AGC TGC CGG AAG AGG GAC TGG AAG AAA CCC GAG TGC AAA GTC AGG    366

 91  P   N   G   R   K   R   K   C   L   A   C   I   K   L   G    105
367 CCC AAT GGG AGG AAA CGG AAA TGC CTG GCC TGC ATC AAA CTG GGC    411

106  S   E   D   K   V   L   G   R   L   V   H   C   P   I   E    120
412 TCT GAG GAC AAA GTT CTG GGC CGG TTG GTC CAC TGC CCC ATA GAG    456

121  T   Q   V   L   R   E   A   E   E   H   Q   E   T   Q   C    135
457 ACC CAA GTT CTG CGG GAG GCT GAG GAG CAC CAG GAG ACC CAG TGC    501

136  L   R   V   Q   R   A   G   E   D   P   H   S   F   Y   F    150
502 CTC AGG GTG CAG CGG GCT GGT GAG GAC CCC CAC AGC TTC TAC TTC    546

151  P   G   Q   F   A   F   S   K   A   L   P   R   S   *        164
547 CCT GGA CAG TTC GCC TTC TCC AAG GCC CTG CCC CGC AGC TAA        588
```

Figure 7: Nucleotide and deduced amino acid sequence of mouse Tig2 (SEQ ID Nos: 9 and 10, respectively)

```
  1  M   K   C   L   L   I   S   L   A   L   W   L   G   T   V      15
102 ATG AAG TGC TTG CTG ATC TCC CTA GCC CTA TGG CTG GGC ACA GTG     146

 16  G   T   R   G   T   E   P   E   L   S   E   T   Q   R   R      30
147 GGC ACA CGT GGG ACA GAG CCC GAA CTC AGC GAG ACC CAG CGC AGG     191

 31  S   L   Q   V   A   L   E   E   F   H   K   H   P   P   V      45
192 AGC CTA CAG GTG GCT CTG GAG GAG TTC CAC AAA CAC CCA CCT GTG     236

 46  Q   L   A   F   Q   E   I   G   V   D   R   A   E   E   V      60
237 CAG TTG GCC TTC CAA GAG ATC GGT GTG GAC AGA GCT GAA GAA GTG     281

 61  L   F   S   A   G   T   F   V   R   L   E   F   K   L   Q      75
282 CTC TTC TCA GCT GGC ACC TTT GTG AGG TTG GAA TTT AAG CTC CAG     326

 76  Q   T   N   C   P   K   K   D   W   K   K   P   E   C   T      90
327 CAG ACC AAC TGC CCC AAG AAG GAC TGG AAA AAG CCG GAG TGC ACA     371

 91  I   K   P   N   G   R   R   R   K   C   L   A   C   I   K     105
372 ATC AAA CCA AAC GGG AGA AGG CGG AAA TGC CTG GCC TGC ATT AAA     416

106  M   D   P   K   G   K   I   L   G   R   I   V   H   C   P     120
417 ATG GAC CCC AAG GGT AAA ATT CTA GGC CGG ATA GTC CAC TGC CCA     461

121  I   L   K   Q   G   P   Q   D   P   Q   E   L   Q   C   I     135
462 ATT CTG AAG CAA GGG CCT CAG GAT CCT CAG GAG TTG CAA TGC ATT     506

136  K   I   A   Q   A   G   E   D   P   H   G   Y   F   L   P     150
507 AAG ATA GCA CAG GCT GGC GAA GAC CCC CAC GGC TAC TTC CTA CCT     551

151  G   Q   F   A   F   S   R   A   L   R   T   K   *             163
552 GGA CAG TTT GCC TTC TCC AGG GCC CTG AGA ACC AAA TAA             590
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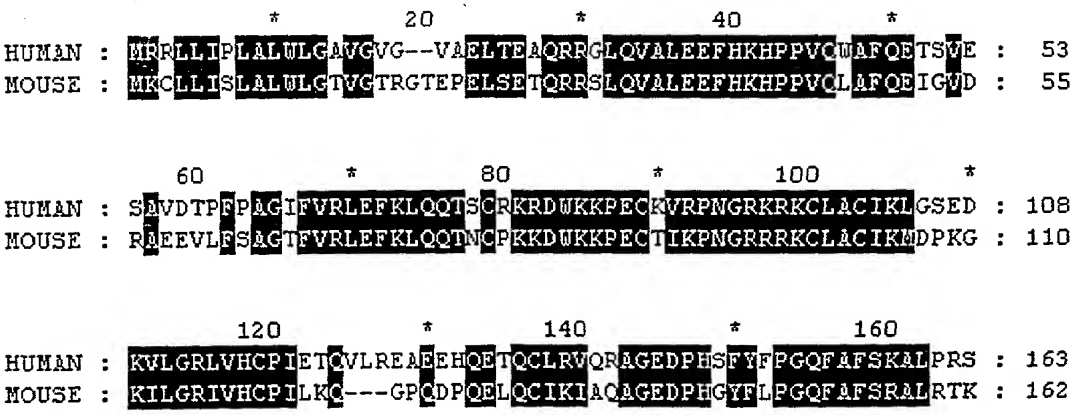
Figure 8: Amino acid sequence alignment of human and mouse TIG2. Identical and similar residues are shaded.



	151	168
mus	HGYFLPGQFA	FSRALRTK
rat	RIYFFPGQFA	FSRAL~~~
tig2	HSFYFPGQFA	FSKALPRS
sus	HSYYFPGQFA	FFKALPPS
bos	HSYYLPGQFA	FIKAL~~~
gallus	DVLYLPGMFA	FSKGLP~~

Identities :

	bos.pep	mus.pep	sus.pep	gallus	rat.pep
tig2.pep	83.750	56.250	86.503	30.675	61.392
bos.pep		54.375	87.500	31.875	56.329
mus.pep			54.375	31.677	73.125
sus.pep				31.288	58.228
gallus.pep					30.818

Figure 11: Primary screening of HPLC fractions obtained from the fractionation of human ovary ascites.

The different fractions obtained following fractionation of human ovary ascites were diluted fivefold in the buffer assay and tested in aequorin assay using a cell line expressing ChemR23 (open circles) or cell lines expressing not related receptors (closed triangles and squares). The response obtained for each fraction was normalized using the ATP response of each cell line.

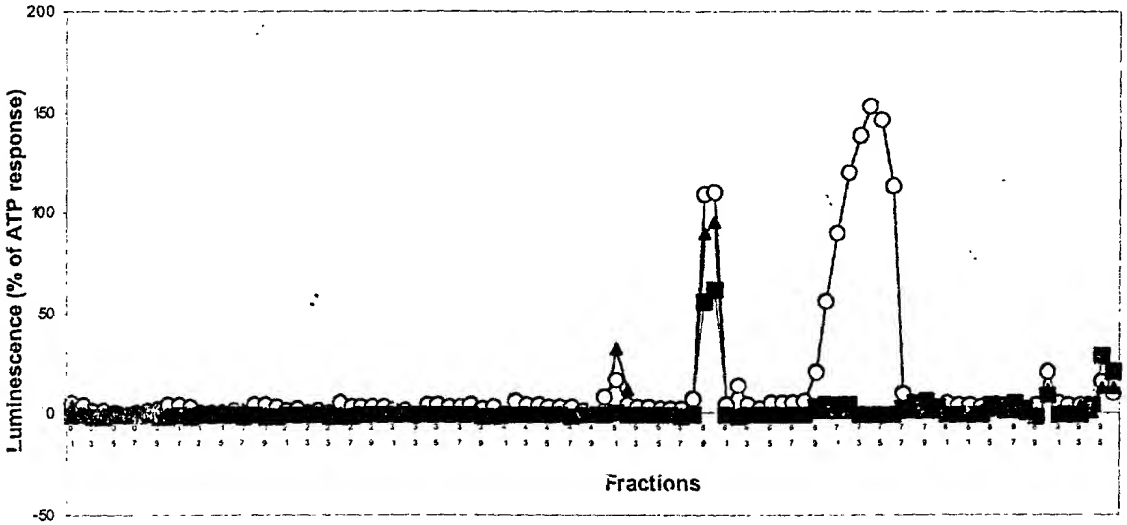


Figure 12: Activation of ChemR23 by cells transfected with TIG2

293 T cells were transiently transfected with pCDNA3- TIG2 or with pCDNA3 alone (mock transfected). Increasing volumes of the supernatant collected 4 days following transfection were analysed in a aequorin-based assay with CHO cells expressing ChemR23. A representative experiment is shown. Assay was performed in triplicate and SD are indicated.

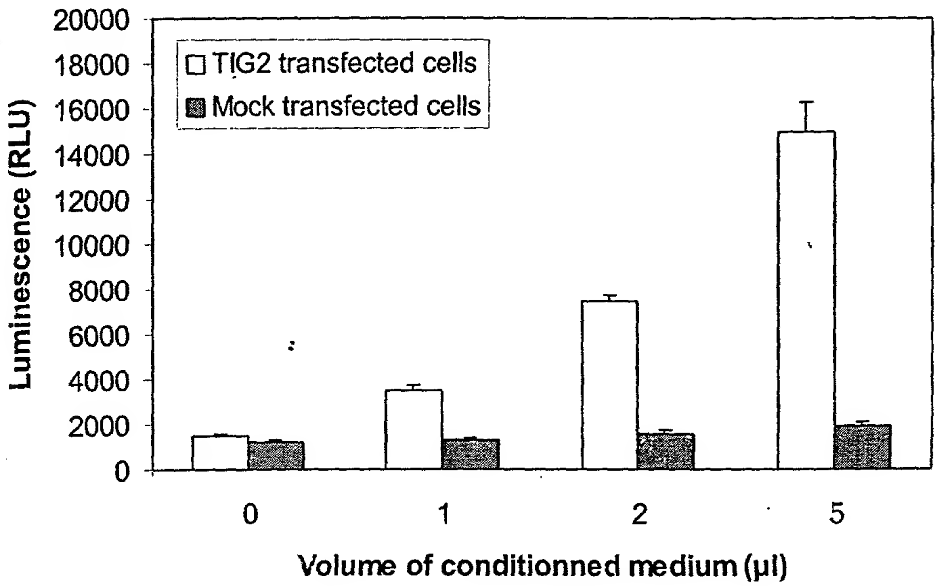


Figure 13: Characterization of antibodies directed against ChemR23
A mixture of recombinant cells made up of 2/3 recombinant ChemR23 CHO cells and 1/3 recombinant HCR CHO cells (negative control) was subject to react with either a supernatant of the anti ChemR23 5C 1H2 monoclonal antibody (thick line) or a supernatant with no known antibody activity (thin line, grey filling). After staining with FITC labeled anti mouse Ig these preparations were analysed by flow cytofluorometry. Results are displayed as a histogram of the number of cells (Events axis) expressing a given fluorescence (FL1-H axis). Monoclonal 5C 1H2 allowed to discriminate the ChemR23 recombinant sub-population of cells from the negative control cells as evidenced by the relative proportions of both type of cells. The background fluorescence of the assay is given by the second staining (grey filling).